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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=3; day=26; hr=10; min=17; sec=4; ms=180; ]

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Reviewer Comments:

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo  
Tadanori Mayumi  
Yasuo Tsutsumi  
Shinsaku Nakagawa

In the second to fourth applicant lines, please use this format:  
Surname, First Name (example: Mayumi, Tadanori).

<210> 1  
<211> 157  
<212> PRT  
<213> human

<400>

Please change the <213> response to "Homo sapiens". Per Section 1.823 of the Sequence Rules, use "Genus species". Please insert a "1" on the <400> line (e.g, <400> 1)

<210> 2  
<211> 471  
<212> DNA  
<213> Artificial Sequence

<400> 2

gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt 48  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
1 5 10 15  
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96

Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	
			20					25					30			
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	
		35					40					45				
gtg	gtg	cca	tca	gag	ggc	ctg	tac	ctc	atc	tac	tcc	cag	gtc	ctc	ttc	192
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	
	50					55				60						
tcg	ggc	caa	ggc	tgc	ccc	tcc	acc	cat	gtg	ctc	ctc	acc	cac	acc	atc	240
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	
	65				70				75					80		
agc	cgc	atc	gcc	gtc	tcc	tac	cag	acc	ccc	gtc	aac	ctc	ctc	tct	gcc	288
Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Pro	Val	Asn	Leu	Leu	Ser	Ala	
			85					90					95			
atc	cgc	agc	ccc	tgc	cag	agg	gag	acc	cca	gag	ggg	gct	gag	gcc	aac	336
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn	
			100				105					110				
ccc	tgg	tat	gag	ccc	atc	tat	ctg	gga	ggg	gtc	ttc	cag	ctg	gag	ccg	384
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro	
	115					120				125						
ggt	gac	cga	ctc	agc	gct	gag	atc	aat	cgg	ccc	gac	tat	ctc	gac	ttt	432
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	
	130					135				140						
gcc	gag	tct	ggg	cag	gtc	tac	ttt	ggg	atc	att	gcc	ctg				
Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu				
145				150					155							

Per 1.823 of the Sequence Rules: if the <213> response is either "Artificial Sequence" or "Unknown", please insert a <220>-<223> section explaining the source of the genetic material. Please insert a cumulative total of "471" at the right margin of the last nucleotide above. These two types of errors appear in many subsequent sequences. Please correct them.

<210> 5  
 <211> 157  
 <212> PRT  
 <213> Artificial Sequence

<400> 5  
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
 1 5 10 15

Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Xaa	Asn	Xaa	Xaa	
			20					25					30			
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	
		35					40					45				
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	
	50					55					60					
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	
65					70					75					80	
Ser	Arg	Ile	Ala	Val	Ser	Tyr	Gln	Thr	Pro	Val	Asn	Leu	Leu	Ser	Ala	
				85					90					95		
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn	
			100					105					110			
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro	
		115					120					125				
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	
	130					135					140					
Xaa	Xaa	Xaa	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu				
145					150					155						

Please: 1) insert a <220>-<223> section explaining "Artificial Sequence"; 2) please explain all Xaa's in a separate <220>-<223> section (which amino acids do they represent?). These two types of errors appear in many subsequent sequences.

<210> 6

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 6

gtc	aga	tca	tct	tct	cga	acc	ccg	agt	gac	atg	cct	gta	gcc	cat	gtt	48
Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Met	Pro	Val	Ala	His	Val	
1				5					10					15		
gta	gca	aac	cct	caa	gct	gag	ggg	cag	ctc	cag	tgg	nns	aac	nns	nns	96
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Xaa	Asn	Xaa	Xaa	
			20					25					30			
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	
		35					40					45				
gtg	gtg	cca	tca	gag	ggc	ctg	tac	ctc	atc	tac	tcc	cag	gtc	ctc	ttc	192
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	

50	55	60	
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc	240		
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile			
65	70	75	80
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc	288		
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala			
85	90	95	
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac	336		
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn			
100	105	110	
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg	384		
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro			
115	120	125	
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt	432		
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe			
130	135	140	
nns nns nns ggg cag gtc tac ttt ggg atc att gcc ctg			
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu			
145	150	155	

Please: 1) explain "Artificial Sequence"; 2) explain all "n's" in a separate <220>-<223> section; which nucleotides do they represent? 3) please insert a cumulative nucleotide total of "471" at the right margin of the last nucleotide line. These three types of errors appear in many subsequent sequences.

<210> 9  
 <211> 157  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Clone No.5

As an explanation of "Artificial Sequence", the above <223> response needs more information regarding its source. Same error in many subsequent sequences.

<210> 83  
 <211> 87  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Oligonucleotide as a primer having NNS sequences (for mutating the amino acid residues at the 29,31 and 32)

<400> 83

gacatgcctg tagcccatgt tgtagcaaac cctcaagctg aggggcagct ccagtgggns 60  
aacnnsnns ccaatgccct cctggcc

The above <223> response exceeds the Sequence Rules' required 72-character line limit; insert a hard return.

Please explain all n's in a separate <220>-<223> section. Please insert a cumulative nucleotide total at the right margin of the last nucleotide line. Same errors in subsequent sequences.

<210> 84

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide as a primer having NNS sequences (for mutating the amino acid residues at the 145 to 147)

<400> 84

cagggcaatg atcccaaagt agacctgcc snnnsnnsna aagtcgagat agtcggg

Please insert a hard return in the <223> response; please correct spelling of "residues" (not "resudues"). What is "at the 145 to 147"? Please explain all n's. Please insert a cumulative nucleotide total at the right margin of the nucleotide line. These errors appear in subsequent sequences.

Please ensure that all subsequent sequences follow the directions above. Suggestion: please consult the Sequence Rules for valid format.

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Application No: 10585296 Version No: 1.0

**Input Set:****Output Set:**

**Started:** 2010-03-16 10:24:54.294  
**Finished:** 2010-03-16 10:25:08.538  
**Elapsed:** 0 hr(s) 0 min(s) 14 sec(s) 244 ms  
**Total Warnings:** 90  
**Total Errors:** 130  
**No. of SeqIDs Defined:** 90  
**Actual SeqID Count:** 90

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
E 201	Mandatory field data missing in <400> SEQID: (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 341	'Xaa' position not defined SEQID (5) POS (29)
E 341	'Xaa' position not defined SEQID (5) POS (31)
E 341	'Xaa' position not defined SEQID (5) POS (32)

**Input Set:**

**Output Set:**

**Started:** 2010-03-16 10:24:54.294

**Finished:** 2010-03-16 10:25:08.538

**Elapsed:** 0 hr(s) 0 min(s) 14 sec(s) 244 ms

**Total Warnings:** 90

**Total Errors:** 130

**No. of SeqIDs Defined:** 90

**Actual SeqID Count:** 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (5) POS (145)
E 341	'Xaa' position not defined SEQID (5) POS (146)
E 341	'Xaa' position not defined SEQID (5) POS (147)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 342	'n' position not defined found at POS: 85 SEQID(6)
E 342	'n' position not defined found at POS: 86 SEQID(6)
E 342	'n' position not defined found at POS: 91 SEQID(6)
E 342	'n' position not defined found at POS: 92 SEQID(6)
E 342	'n' position not defined found at POS: 94 SEQID(6)
E 342	'n' position not defined found at POS: 95 SEQID(6)
E 341	'Xaa' position not defined SEQID (6) POS (29)
E 341	'Xaa' position not defined SEQID (6) POS (31)
E 341	'Xaa' position not defined SEQID (6) POS (32)
E 342	'n' position not defined found at POS: 433 SEQID(6)
E 342	'n' position not defined found at POS: 434 SEQID(6)
E 342	'n' position not defined found at POS: 436 SEQID(6)
E 342	'n' position not defined found at POS: 437 SEQID(6)
E 342	'n' position not defined found at POS: 439 SEQID(6)
E 342	'n' position not defined found at POS: 440 SEQID(6)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(6)

**Input Set:**

**Output Set:**

**Started:** 2010-03-16 10:24:54.294  
**Finished:** 2010-03-16 10:25:08.538  
**Elapsed:** 0 hr(s) 0 min(s) 14 sec(s) 244 ms  
**Total Warnings:** 90  
**Total Errors:** 130  
**No. of SeqIDs Defined:** 90  
**Actual SeqID Count:** 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (6) POS (145)
E 341	'Xaa' position not defined SEQID (6) POS (146)
E 341	'Xaa' position not defined SEQID (6) POS (147)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 341	'Xaa' position not defined SEQID (7) POS (84)
E 341	'Xaa' position not defined SEQID (7) POS (85)
E 341	'Xaa' position not defined SEQID (7) POS (86)
E 341	'Xaa' position not defined SEQID (7) POS (87)
E 341	'Xaa' position not defined SEQID (7) POS (88)
E 341	'Xaa' position not defined SEQID (7) POS (89)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 342	'n' position not defined found at POS: 250 SEQID(8)
E 342	'n' position not defined found at POS: 251 SEQID(8)
E 342	'n' position not defined found at POS: 253 SEQID(8)
E 342	'n' position not defined found at POS: 254 SEQID(8)
E 342	'n' position not defined found at POS: 256 SEQID(8)
E 342	'n' position not defined found at POS: 257 SEQID(8)
E 342	'n' position not defined found at POS: 259 SEQID(8)
E 342	'n' position not defined found at POS: 260 SEQID(8)
	This error has occurred more than 20 times, will not be displayed



**Input Set:**

**Output Set:**

**Started:** 2010-03-16 10:24:54.294

**Finished:** 2010-03-16 10:25:08.538

**Elapsed:** 0 hr(s) 0 min(s) 14 sec(s) 244 ms

**Total Warnings:** 90

**Total Errors:** 130

**No. of SeqIDs Defined:** 90

**Actual SeqID Count:** 90

Error code	Error Description
E 341	'Xaa' position not defined SEQID (8) POS (84)
E 341	'Xaa' position not defined SEQID (8) POS (85) This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(23)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 441 SEQID(24)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(25)

**Input Set:**

**Output Set:**

**Started:** 2010-03-16 10:24:54.294  
**Finished:** 2010-03-16 10:25:08.538  
**Elapsed:** 0 hr(s) 0 min(s) 14 sec(s) 244 ms  
**Total Warnings:** 90  
**Total Errors:** 130  
**No. of SeqIDs Defined:** 90  
**Actual SeqID Count:** 90

Error code	Error Description
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(26)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(27)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(28)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(29)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(30)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(31)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(32)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(33)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(34)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(35)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(36)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 471 SEQID(60) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo  
Tadanori Mayumi  
Yasuo Tsutsumi  
Shinsaku Nakagawa

<120> TNF antagonist and TNF inhibitor containing it as an effective ingredient

<130> WO1042

<140> 10585296  
<141> 2010-03-16

<160> 90

<210> 1  
<211> 157  
<212> PRT  
<213> human

<400>  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val  
1 5 10 15  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
20 25 30  
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
85 90 95  
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
100 105 110  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys  
115 120 125  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140  
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 2  
<211> 471  
<212> DNA  
<213> Artificial Sequence

<400> 2  
gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt 48  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
1 5 10 15  
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
20 25 30  
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240  
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc 288  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala  
85 90 95  
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac 336  
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn  
100 105 110  
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg 384  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro  
115 120 125  
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140  
gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg  
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 3  
<211> 471  
<212> DNA  
<213> Artificial Sequence

<400> 3  
gtc aga tca tct tct cga acc ccg agt gac gcg cct gta gcc cat gtt 48  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Ala Pro Val Ala His Val  
1 5 10 15  
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg 96  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg  
20 25 30  
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144  
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240  
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
agc cgc atc gcc gtc tcc tac cag acc cgg gtc aac ctc ctc tct gcc 288  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Arg Val Asn Leu Leu Ser Ala  
85 90 95  
atc gcc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc ctc 336  
Ile Ala Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Leu  
100 105 110  
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag acc 384  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Thr  
115 120 125  
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe

130	135	140
gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg		
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu		
145	150	155

<210> 4  
 <211> 471  
 <212> DNA  
 <213> Artificial Sequence

<400> 4

gtc aga tca tct tct cga acc ccg agt gac gcg cct gta gcc cat gtt	48
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Ala Pro Val Ala His Val	
1 5 10 15	
gta gca aac cct caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg	96
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg	
20 25 30	
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg	144
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu	
35 40 45	
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc	192
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe	
50 55 60	
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc	240
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile	
65 70 75 80	
agc cgc atc gcc gtc tcc tac cag acc gac gtc aac ctc ctc tct gcc	288
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala	
85 90 95	
atc gcc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc ctc	336
Ile Ala Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Leu	
100 105 110	
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag acc	384
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Thr	
115 120 125	
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt	432
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe	
130 135 140	
gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg	
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	
145 150 155	

<210> 5  
 <211> 157  
 <212> PRT  
 <213> Artificial Sequence

<400> 5

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Xaa Asn Xaa Xaa
20 25 30
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe

50	55	60
Ser Gly Gln Gly Cys Pro	Ser Thr His Val Leu	Leu Thr His Thr Ile
65	70	75
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala		80
	85	90
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn		95
	100	105
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro		110
	115	120
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe		125
	130	135
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu		140
145	150	155

<210> 6  
 <211> 471  
 <212> DNA  
 <213> Artificial Sequence

<400> 6

gtc aga tca tct tct cga acc ccg agt gac atg cct gta gcc cat gtt 48
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val
1 5 10 15
gta gca aac cct caa gct gag ggg cag ctc cag tgg nns aac nns nns 96
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Xaa Asn Xaa Xaa
20 25 30
gcc aat gcc ctc ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg 144
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45
gtg gtg cca tca gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc 192
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60
tcg ggc caa ggc tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc 240
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80
agc cgc atc gcc gtc tcc tac cag acc ccc gtc aac ctc ctc tct gcc 288
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala
85 90 95
atc cgc agc ccc tgc cag agg gag acc cca gag ggg gct gag gcc aac 336
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn
100 105 110
ccc tgg tat gag ccc atc tat ctg gga ggg gtc ttc cag ctg gag ccg 384
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro
115 120 125
ggt gac cga ctc agc gct gag atc aat cgg ccc gac tat ctc gac ttt 432
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140
nns nns nns ggg cag gtc tac ttt ggg atc att gcc ctg
Xaa Xaa Xaa Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 7  
 <211> 157  
 <212> PRT  
 <213> Artificial Sequence

<400> 7

Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Met	Pro	Val	Ala	His	Val
1				5					10					15	
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg
			20					25					30		
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu
			35				40					45			
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe
	50					55					60				
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile
65				70						75					80
Ser	Arg	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Val	Asn	Leu	Leu	Ser	Ala
			85						90					95	
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn
			100					105					110		
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro
	115					120					125				
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe
	130					135					140				
Ala	Glu	Ser	Gly	Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu			
145					150					155					

<210> 8

<211> 471

<212> DNA

<213> Artificial Sequence

<400> 8

gtc	aga	tca	tct	tct	cga	acc	ccg	agt	gac	atg	cct	gta	gcc	cat	gtt	48
Val	Arg	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Asp	Met	Pro	Val	Ala	His	Val	
1				5					10					15		
gta	gca	aac	cct	caa	gct	gag	ggg	cag	ctc	cag	tgg	ctg	aac	cgc	cgg	96
Val	Ala	Asn	Pro	Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	
			20					25					30			
gcc	aat	gcc	ctc	ctg	gcc	aat	ggc	gtg	gag	ctg	aga	gat	aac	cag	ctg	144
Ala	Asn	Ala	Leu	Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	
			35				40					45				
gtg	gtg	cca	tca	gag	ggc	ctg	tac	ctc	atc	tac	tcc	cag	gtc	ctc	ttc	192
Val	Val	Pro	Ser	Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	
	50					55					60					
tcg	ggc	caa	ggc	tgc	ccc	tcc	acc	cat	gtg	ctc	ctc	acc	cac	acc	atc	240
Ser	Gly	Gln	Gly	Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	
65				70						75					80	
agc	cgc	atc	nns	nns	nns	nns	nns	nns	ccc	gtc	aac	ctc	ctc	tct	gcc	288
Ser	Arg	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Val	Asn	Leu	Leu	Ser	Ala	
			85						90					95		
atc	cgc	agc	ccc	tgc	cag	agg	gag	acc	cca	gag	ggg	gct	gag	gcc	aac	336
Ile	Arg	Ser	Pro	Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Asn	
			100					105					110			
ccc	tgg	tat	gag	ccc	atc	tat	ctg	gga	ggg	gtc	ttc	cag	ctg	gag	ccg	384
Pro	Trp	Tyr	Glu	Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Pro	
	115					120						125				
ggt	gac	cga	ctc	agc	gct	gag	atc	aat	cgg	ccc	gac	tat	ctc	gac	ttt	432
Gly	Asp	Arg	Leu	Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	
	130					135					140					

gcc gag tct ggg cag gtc tac ttt ggg atc att gcc ctg  
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 9  
<211> 157  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone No.5

<400> 9  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
1 5 10 15  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Arg Asn Ser His  
20 25 30  
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala  
85 90 95  
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn  
100 105 110  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro  
115 120 125  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140  
Ser Gly Thr Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 10  
<211> 146  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone No.6

<400> 10  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
1 5 10 15  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Ser Asn Arg Tyr  
20 25 30  
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala  
85 90 95



Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn  
100 105 110  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro  
115 120 125  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140  
Ser Met  
145

<210> 11  
<211> 157  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Clone No.7

<400> 11  
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Met Pro Val Ala His Val  
1 5 10 15  
Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp His Asn Asn Thr  
20 25 30  
Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu  
35 40 45  
Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60  
Ser Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80  
Ser Arg Ile Ala Val Ser Tyr Gln Thr Pro Val Asn Leu Leu Ser Ala  
85 90 95  
Ile Arg Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Asn  
100 105 110  
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Pro  
115 120 125  
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140  
Asp Ser Asn Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145 150 155

<210> 12  
<211> 157  
<212> PRT  
<213> Artifici